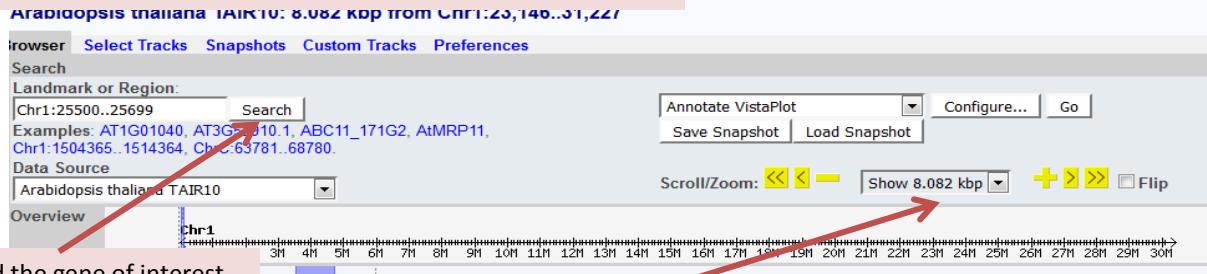
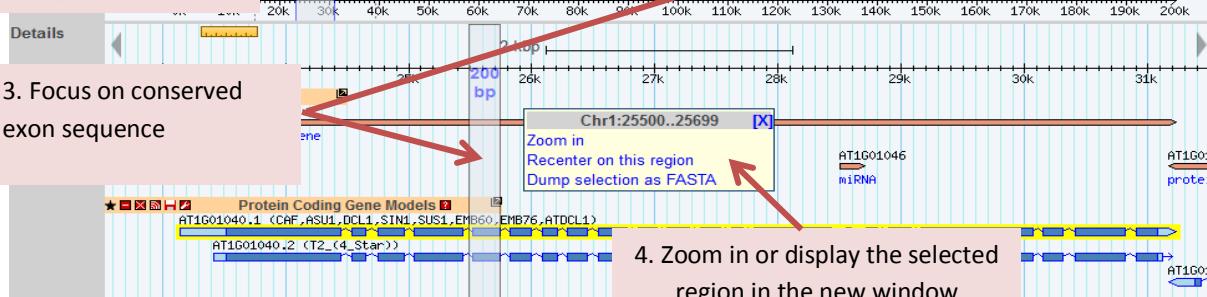


1. Go to TAIR10 genome browser:

<http://www.arabidopsis.org/servlets/tools/gbrowse/arabidopsis>

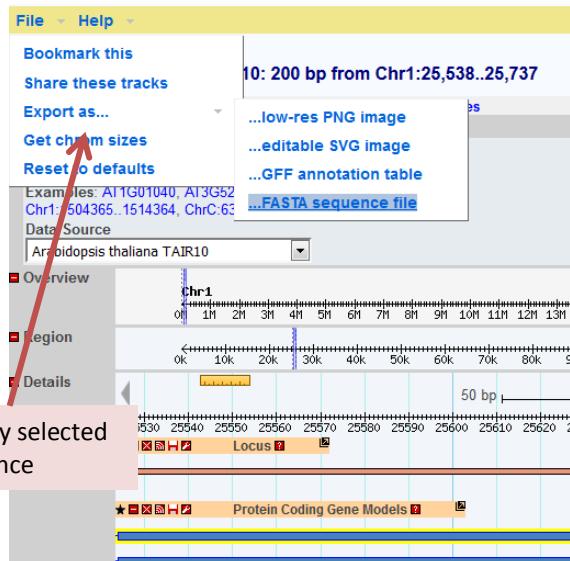


2. Find the gene of interest



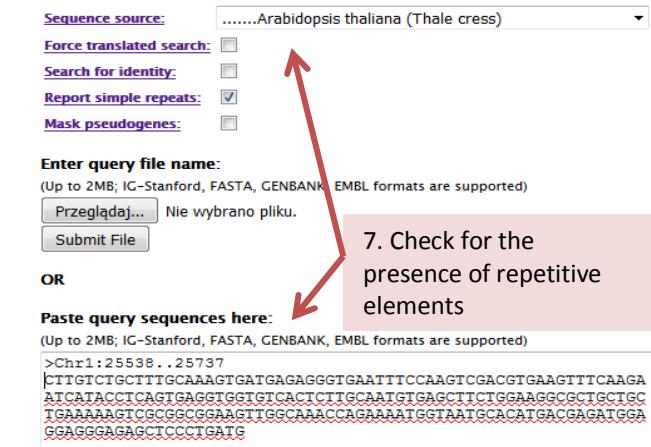
3. Focus on conserved exon sequence

4. Zoom in or display the selected region in the new window



5. Copy selected sequence

6. Go to CENSOR tool: <http://www.girinst.org/censor/>



7. Check for the presence of repetitive elements

8. Go to 1001 Genomes site: <http://tools.1001genomes.org/>

VCF Download

Download Subsets of 1001 VCF Files. [More...](#)

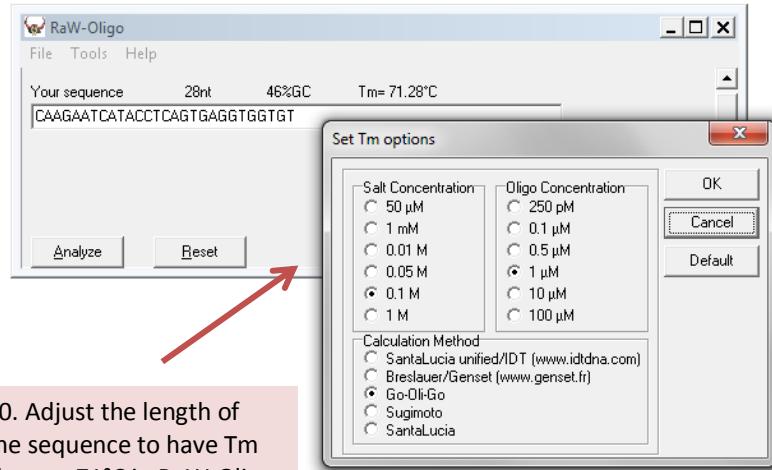
Select Strains Select Loci Select Formats Start Download

Please select a set of strains.

<input type="checkbox"/>	Ecotype ID	Name	CS Number	Country	Group
<input checked="" type="checkbox"/>	1001U	Sj-4	CS76381	UZB	asia
<input checked="" type="checkbox"/>	10015	Ara-1	CS76382	AFG	asia
<input checked="" type="checkbox"/>	9953	Koz-2	CS76383	RUS	asia
<input checked="" type="checkbox"/>	9952	Ko-4	CS76384	RUS	asia
<input checked="" type="checkbox"/>	9951	Ko-1	CS76385	RUS	asia
<input checked="" type="checkbox"/>	10014	Xan-1	CS76387	AZE	italy_balkan_caucasus
<input checked="" type="checkbox"/>	10013	Lerik1-3	CS76388	AZE	italy_balkan_caucasus
<input checked="" type="checkbox"/>	10012	Istisu-1	CS76389	AZE	italy_balkan_caucasus
<input checked="" type="checkbox"/>	9990	Lag2-2	CS76390	GEO	italy_balkan_caucasus
<input checked="" type="checkbox"/>	9991	Vash-1	CS76391	GEO	italy_balkan_caucasus
<input checked="" type="checkbox"/>	9988	Bak-2	CS76392	GEO	italy_balkan_caucasus
<input checked="" type="checkbox"/>	10011	Yen-1	CS76394	ARM	asia

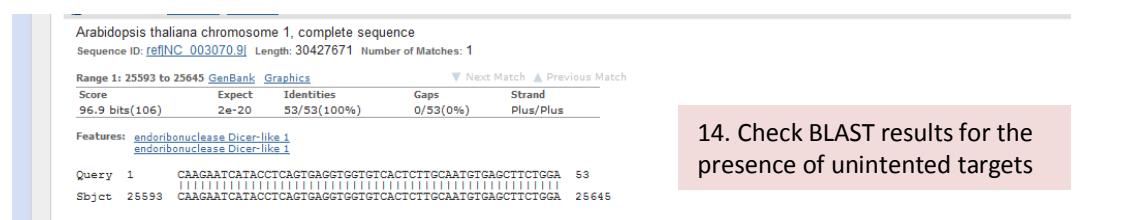
9. Download and evaluate the SNP data for selected region and accession

Supplementary Figure S1. The schematic procedure of the MLPA half-probes design



11. Go to: <http://blast.ncbi.nlm.nih.gov/Blast.cgi> Select Nucleotide BLAST

The NCBI BLASTN interface shows a query sequence input field containing the joined sequence CAAGAACATACCTCAGTGAGGTGGTGT. The 'Choose Search Set' section is highlighted with a yellow background, showing 'Database' set to 'Human genomic + transcript' and 'NCBI Genomes (chromosome)' selected. The 'Program Selection' section shows 'Optimize for' set to 'Somewhat similar sequences (blastn)'. A red arrow points from the text '12. Paste the joined sequence of paired TSSs' to the query sequence input field. Another red arrow points from the text '13. Select the parameters' to the 'Choose Search Set' section. A third red arrow points from the text '13. Select the parameters' to the 'Program Selection' section.



15. Use the MS Excel template to add primer and stuffer sequence and design the final half-probes

Left TSS	Tm of Left TSS	Range of Acceptable Left TSS Lengths	Left TSS Length	Left TSS Length Correct?	Left Half-Probe Sequence	Left Half-Probe Length	Anticipated Left Half-Probe Length	Left Half-Probe Correct?
CAAGAACATACCTCAGTGAGGTGGTGT	71,28	21-26	0	Not Used	Not Used	0	45	Not Used
		21-27	0	Not Used	Not Used	0	46	Not Used
		21-29	28	Yes	GGGTTCCCTAAGGGTTGGACCAAGAA	48	48	Yes
		21-30	0	Not Used	Not Used	0	49	Not Used
		21-32	0	Not Used	Not Used	0	51	Not Used

Supplementary Figure S1 (Continued).